

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 18:51:30 ; Search time 194 Seconds
(without alignments)
525.563 Million cell updates/sec

Title: US-10-665-602-2
Perfect score: 223
Sequence: 1 MTRHHVRLFTVSLALQII.....PSVLQRERRPCGRPLGLHRL 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 6

Total number of hits satisfying chosen parameters: 14456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq 8:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
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- 6: Geneseqp2003as:*
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- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*
- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	223	100.0	223	8	Ado05060 Human cri
2	223	100.0	223	4	Aau18122 Novel hum
3	223	100.0	229	4	Aau17028 Human nov
4	223	100.0	229	4	Abb10300 Human cdn
5	223	100.0	229	4	Aau19904 Novel hum
6	223	100.0	229	5	Abj05749 Novel hum
7	223	100.0	229	5	Abp66887 Human pol
8	187	83.9	223	5	Abb90336 Human pol
9	187	83.9	223	6	Abu56711 Lung canc
10	187	83.9	223	7	Adn39104 Cancer/an
11	187	83.9	223	7	Adn39975 Cancer/an
12	187	83.9	223	9	Ady85963 Human cri
13	187	83.9	231	4	Aau16957 Human nov
14	149	66.8	230	2	Aaw09111 Human cri
15	145	65.0	223	5	Aag77914 Human cry
16	15	6.7	202	9	Ady85962 Murine cr
17	14	6.3	14	4	Aam00665 Human pro
18	8	3.6	60	4	Aam06349 Human foe
19	8	3.6	64	4	Aam06772 Human foe
20	8	3.6	120	4	Aao10911 Human pol
21	8	3.6	158	4	Abb68713 Drosophil
22	8	3.6	180	4	Aam99763 Human exc
23	8	3.6	180	4	Aam42398 Human pol

24	8	3.6	180	4	AAM42578	Human kid
25	8	3.6	333	7	ABM86084	Rice abio
26	8	3.6	334	8	ADU02861	Novel hum
27	8	3.6	363	7	ABO69270	Pseudomon
28	8	3.6	420	6	ABU11822	Human MDD
29	8	3.6	575	8	ADY08754	Plant ful
30	8	3.6	575	8	ADY12991	Plant ful
31	8	3.6	737	8	ADY08040	Plant ful
32	8	3.6	788	8	ADO55178	Protein #
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34	8	3.6	1230	7	ADE60957	Human Pro
35	8	3.6	1230	7	ADD45964	Human Pro
36	8	3.6	1253	4	ABG23851	Novel hum
37	8	3.6	1718	5	AAE26420	Human tra
38	8	3.6	2523	8	ADL26915	Xenopus s
39	7	3.1	21	9	ADV55161	G protein
40	7	3.1	22	7	ADE28537	Human CD1
41	7	3.1	24	5	ABB74254	Fusogenic
42	7	3.1	27	4	AAE03135	Human gen
43	7	3.1	30	9	ADZ77602	Human MHC
44	7	3.1	33	9	ADY28315	Novel Erb
45	7	3.1	38	4	AAO03363	Human pol

ALIGNMENTS

RESULT 1

AD005060	ID	AD005060 standard; protein; 223 AA.
XX	AC	AD005060;
XX	DT	29-JUL-2004 (first entry)
XX	DE	Human criptin growth factor (CGF) protein.
XX	KW	Criptin growth factor; CGF; wound healing; tissue regeneration;
KW	KM	implant fixation; angiogenesis; neoplasia; tumour; gene therapy; human.
XX	OS	Homo sapiens.
XX	PN	US2004086967-A1.
XX	PD	06-MAY-2004.
XX	PF	22-SEP-2003; 2003US-00665602.
XX	PR	06-JUN-1995; 95US-00471371.
PR	09-SEP-1999;	99US-00393023.
XX	(HUMA-)	HUMAN GENOME SCI INC.
XX	PA	Meissner PS, Coleman TA;
XX	PI	WPI; 2004-356201/33.
XX	DR	N-PSDB; ADO05059.
XX	PT	New human polynucleotides encoding human criptin growth factor
PT	PT	polypeptides, useful for wound healing or tissue regeneration,
PT	PT	stimulating implant fixation and angiogenesis, and for treating and/or
PT	PT	preventing tumor.
XX	PS	Claim 12; SEQ ID NO 2; 19pp; English.
XX	CC	The invention provides criptin growth factor (CGF) polypeptides and their
CC	CC	encoding polynucleotides. The invention is useful for wound healing and
CC	CC	tissue regeneration, stimulating implant fixation, angiogenesis and for
CC	CC	treating and preventing neoplasia such as tumour. The invention is also
CC	CC	useful in gene therapy. The present sequence is human criptin growth
XX	XX	factor (CGF) protein.
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ID	AAU18122 standard; protein; 229 AA.				
XX	AAU18122;				
AC					
DT	21-NOV-2001 (first entry)				
XX					
DE	Novel human uterine motility-association polypeptide #29.				
XX					
KW	Human; uterine motility-association disorder; uterus; pregnancy; labour;				
KW	menstrual cycle; gene therapy.				
XX					
OS	Homo sapiens.				
XX					
PN	W020015201-A1.				
XX					
PD	02-AUG-2001.				
XX					
PF	17-JAN-2001; 2001WO-US001317.				
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PR 11-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WFI; 2001-488777/53.
XX N-PSDB; AAS28964.
XX
XX New nucleic acid molecules encoding 49 human secreted proteins for
XX diagnosing, preventing, treating or ameliorating medical conditions and
XX used as food additives or preservatives.
XX
XX Claim 11; SEQ ID NO 98; 524pp; English.
XX
XX The present invention relates to the isolation of novel human uterine
XX motility-association polypeptides, and cDNA (AAS28936-AAS28994) and
XX genomic sequences encoding for these polypeptides. The sequences of the
XX invention are useful in the diagnosis, treatment, prevention and/or
XX prognosis of diseases associated with uterine motility such as pregnancy
XX and labour, and menstrual disorders. The polynucleotide sequences of the
XX invention are also useful in gene therapy. AAU18094-AAU18152 represent
XX novel human uterine motility-association polypeptides. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
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XX Sequence 229 AA;
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XX Query Match 100.0%; Score 223; DB 4; Length 229;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-195;
XX Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 7 MTRHHVRLFTVSLAQIINLNGSYQREKHNGRGEVTKVATQKHQSPINWTSSHFGE 66
XX
XX 61 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQR 120
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XX 67 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQR 126
XX
QY 121 SECCALEHGAWTLRACHLCRCIFGALHCLPLQTFDRCDPKDFLASHAHGFSAGGAPSLLL 180
DB 127 SECCALEHGAWTLRACHLCRCIFGALHCLPLQTFDRCDPKDFLASHAHGFSAGGAPSLLL 186
QY 181 LLPCALLHRLLRDPDAPAHPRSLVPSVLQRRRRCGRPLGHLRL 223
DB 187 LLPCALLHRLLRDPDAPAHPRSLVPSVLQRRRRCGRPLGHLRL 229
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ID AAU17028 standard; protein; 229 AA.
XX
XX AAU17028;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human novel secreted protein, SEQ ID 269.
XX
XX Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
XX cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
XX antibacterial; virucide; fungicide; ophthalmological; vulnerary;
XX secreted protein; rheumatoid arthritis; hyperproliferative disorder;
XX cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
XX cerebral ischaemia; angiogenesis; nervous system disorder;
XX Alzheimer's disease; infection; ocular disorder; corneal infection;
XX wound healing; epithelial cell proliferation; skin ageing; food additive;
XX preservative; antiproliferative.
XX
XX Homo sapiens.
XX
XX WO200155441-A2.
XX
XX 02-AUG-2001.
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XX 17-JAN-2001; 2001WO-US001320.
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XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
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PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476222/51.

N-PSDB; AAS26933.

Novel polypeptides and polynucleotides useful as diagnostic reagents to
diagnose diseases or disorders associated with aberrant expression or
activity of polypeptides, for treating blood clotting disorder,
hemophilia.

Claim 11; SEQ ID NO 269; 601pp; English.

The invention relates to isolated nucleic acid molecules and their
encoded secreted proteins. The nucleic acids and proteins are used to
prevent, treat or ameliorate a medical condition in e.g. humans, mice,
rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
in diagnosing a pathological condition or susceptibility to a
pathological condition. Antibodies to the proteins can also be used in
alleviating symptoms associated with the disorders and in diagnostic
immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays
(ELISA). Disorders which are diagnosed or treated include autoimmune
diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
nervous system disorders e.g. Alzheimer's disease, infections caused by
bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
and many other disorders listed in the specification. The polypeptides
can also be used to aid wound healing and epithelial cell proliferation,
to prevent skin aging due to sunburn, to maintain organs before
transplantation, for supporting cell culture of primary tissues, to
regenerate tissues and in chemotaxis. The polypeptides can also be used
as a food additive or preservative to increase or decrease storage
capabilities, fat content, lipid, protein, carbohydrate, vitamins,
minerals, cofactors and other nutritional components. The present
sequence represents a novel secreted protein of the invention. Note: The

Query Match 100.0%; Score 223; DB 4; Length 229;

Best Local Similarity 100.0%; Pred. No. 1.5e-195;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRRHHVRLFTVSLALQIINLGNYSQREKNGRGVEVTKVATQKHSPLNWTSSHFGE 60

Db 7 MTRRHHVRLFTVSLALQIINLGNYSQREKNGRGVEVTKVATQKHSPLNWTSSHFGE 66

Qy	61	VTSAEGWPEEPLPYSAFGEASAPRCRNGGTCVLGSCFVCVPAHFTGRYCEHDQRR	120	PR	01-SEP-2000;	2000US-0229287P.
				PR	01-SEP-2000;	2000US-0229343P.
Db	67	VTSAEGWPEEPLPYSAFGEASAPRCRNGGTCVLGSCFVCVPAHFTGRYCEHDQRR	126	PR	01-SEP-2000;	2000US-0229345P.
				PR	05-SEP-2000;	2000US-0229509P.
Qy	121	SECGALSHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL	180	PR	05-SEP-2000;	2000US-0229513P.
				PR	06-SEP-2000;	2000US-0230437P.
Db	127	SECGALSHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL	186	PR	06-SEP-2000;	2000US-0230438P.
				PR	08-SEP-2000;	2000US-0231242P.
Qy	181	LLPCALLHRLRPDAPAHPSLVPSVLQRRRCGRGLGHRL	223	PR	08-SEP-2000;	2000US-0231243P.
				PR	08-SEP-2000;	2000US-0231244P.
Db	187	LLPCALLHRLRPDAPAHPSLVPSVLQRRRCGRGLGHRL	229	PR	08-SEP-2000;	2000US-0231413P.
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RESULT 4						
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XX	AC	ABB10300;		PR	14-SEP-2000;	2000US-0232398P.
XX	DT	10-JAN-2002 (first entry)		PR	14-SEP-2000;	2000US-0232399P.
XX	DE	Human cDNA SEQ ID NO: 608.		PR	14-SEP-2000;	2000US-0232400P.
XX	KW	Human; gene therapy; neural disorder; immune system disorder;		PR	14-SEP-2000;	2000US-0232401P.
KW	KW	muscular disorder; reproductive disorder; gastrointestinal disorder;		PR	14-SEP-2000;	2000US-0233063P.
KW	KW	pulmonary disorder; cardiovascular disorder; renal disorder;		PR	14-SEP-2000;	2000US-0233064P.
XX	XX	proliferative disorder; inflammation.		PR	14-SEP-2000;	2000US-0233065P.
OS	OS	Homo sapiens.		PR	21-SEP-2000;	2000US-0233423P.
XX	PN	WO200154474-A2.		PR	21-SEP-2000;	2000US-0234274P.
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XX	PF	17-JAN-2001; 2001WO-US001349.		PR	25-SEP-2000;	2000US-0234998P.
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PR 14-SEP-2000; 2000US-0232397P.
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PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254057P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465568/50.
XX N-PSDB; AAS31589.
XX
XX Isolated nucleic acid molecule encoding a calcium-binding protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
XX Claim 11; SEQ ID NO 101; 542pp; English.
XX
XX The present invention relates to the isolation of novel human calcium-
XX binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences
XX encoding for these proteins. The sequences of the invention are useful in
XX the diagnosis, prevention and/or prognosis of diseases associated with
XX aberrant calcium flux. Such disorders include neurological diseases (e.g.
XX amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe
XX combined immunodeficiency, SCID), digestive disorders (e.g. irritable
XX bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders
XX (e.g. haemophilia), and/or infectious disease (e.g. acquired
XX immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are
XX also useful as screening tools to identify antagonists and/or agonists
XX that may enhance or inhibit activities mediated by calcium-binding
XX proteins. The polynucleotides of the invention are also useful in gene
XX therapy. AAU19892-AAU19969 represent the novel human calcium-binding
XX proteins. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 229 AA;
XX
XX Query Match 100.0%; Score 223; DB 4; Length 229;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-195; Indels 0; Gaps 0;
XX Matches 223; Conservative 0; Mismatches 0;
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XX Qy 1 MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGVTKVATQKHROSPLNMTSSHFG 60
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XX Db 7 MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGVTKVATQKHROSPLNMTSSHFG 66
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Qy 61 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRNGGTCVLGSCFVCPAHTGRYCEHQR 120
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 67 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRNGGTCVLGSCFVCPAHTGRYCEHQR 126
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Qy 121 SEGCALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSL 180
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XX Db 127 SEGCALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSL 186
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XX Qy 181 LLPCALHLRLRPDAPAHPRSLVPSVLQRRRRCGFRGLGHLR 223
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XX Db 187 LLPCALHLRLRPDAPAHPRSLVPSVLQRRRRCGFRGLGHLR 229
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XX
XX RESULT 6
XX ABJ05749
XX ID ABJ05749 standard; protein; 229 AA.
XX
XX AC ABJ05749;
XX
XX DT 14-NOV-2002 (first entry)
XX
XX
```

DE XX Novel human protein SEQ ID No 98.

KW Immunostimulant; antirheumatic; antiarthritic; neuroprotective;

KW antiallergic; antidiabetic; antiasthmatic; antiinflammatory; nootropic;

KW immunosuppressive; anticoagulant; thrombolytic; antiatherosclerotic;

KW cytosstatic; nephroprotective; antiparkinsonian; gynecological; virucide;

KW antibacterial; antiarrhythmic; fungicide; HCFAT05; HMAAE95; HTNBM01;

KW immunodeficiency; autoimmune disorder; allergic reaction; cardiovascular;

KW inflammatory condition; graft-versus-host disease; reproductive system;

KW blood-related disorder; hyperproliferative; endocrine; neurological;

KW respiratory; renal; infectious disease; gastrointestinal; gene therapy;

KW neuronal growth; neuronal disorder; neuro-degenerative condition;

KW keratinocyte growth; human.

OS Homo sapiens.

XX US2002086330-A1.

XX 04-JUL-2002.

XX 17-JAN-2001; 2001US-00764893.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 28-JUN-2000; 2000US-0214886P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 14-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 22-AUG-2000; 2000US-0225758P.

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XX 30-AUG-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0229287P.

XX 01-SEP-2000; 2000US-0229343P.

XX 01-SEP-2000; 2000US-0229344P.

XX 01-SEP-2000; 2000US-0229345P.

XX 05-SEP-2000; 2000US-0229509P.

XX 05-SEP-2000; 2000US-0229513P.

XX 08-SEP-2000; 2000US-0231413P.

XX 21-SEP-2000; 2000US-0234223P.

XX 21-SEP-2000; 2000US-0234274P.

XX 25-SEP-2000; 2000US-0234997P.

XX 27-SEP-2000; 2000US-0235834P.

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XX 13-OCT-2000; 2000US-0239935P.

XX 20-OCT-2000; 2000US-0240960P.

XX 20-OCT-2000; 2000US-0241785P.

XX 20-OCT-2000; 2000US-0241809P.

XX 01-NOV-2000; 2000US-0244617P.

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XX 08-DEC-2000; 2000US-0251856P.

XX 08-DEC-2000; 2000US-0251868P.

XX 08-DEC-2000; 2000US-0251869P.

XX

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

XX (BARA/) BARASH S C.

XX Rosen CA, Ruben SM, Barash SC;

XX WPI; 2002-665432/71.

XX Novel polypeptide useful for diagnosis, prognosis, prevention, and

PT treatment of immune, hyperproliferative, renal, respiratory,

PT cardiovascular, reproductive, endocrine, gastrointestinal and

PT neurological disorders.

XX Disclosure; Page 268-269; 335pp; English.

XX The invention relates to an isolated polypeptide comprising a sequence at

CC least 90% identical to a full length protein sequence selected from 55

CC sequences given in the specification such as a sequence of 163, 74 or 140

CC amino acids fully defined in the specification, or the encoding sequence

CC contained in 49 cDNA clones given in specification e.g. HCFAT05, HMAAE95

CC or HTNBM01. The protein and its encoding nucleic acid are useful for

CC diagnosing a pathological condition or susceptibility to a pathological

CC condition in a subject and for preventing, treating or ameliorating a

CC medical condition. The protein, its encoding nucleic acid and an isolated

CC antibody that can bind to the protein are useful in treating, preventing,

CC diagnosing and/or prognosing immunodeficiencies, autoimmune disorders,

CC allergic reactions and conditions, inflammatory conditions, graft-versus-

CC renal disorders, cardiovascular disorders, respiratory disorders,

CC neurological disorders, endocrine disorders, reproductive system

CC disorders, infectious diseases, and gastrointestinal disorders. The

CC protein of the invention is useful to stimulate neuronal growth and to

CC treat, prevent, and/or diagnose neuronal damage which occurs in certain

CC neuronal disorders or neuro-degenerative conditions, for stimulating

CC keratinocyte growth, to prevent hair loss, to modulate mammalian

CC characteristics such as body height, weight, hair color, and to increase

CC or decrease storage capabilities, fat content, lipid, protein,

CC carbohydrate, vitamins, minerals, cofactors or other nutritional

CC components. The nucleic acid of the invention can be used in gene

CC therapy. This sequence represents a novel human protein of the invention

XX

SQ Sequence 229 AA;

Query Match 100.0%; Score 223; DB 5; Length 229;

Best Local Similarity 100.0%; Pred. No. 1.5e-195;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRRHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHRSPLNWTSSHFG 60

DB 7 MTRRHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHRSPLNWTSSHFG 66

QY 61 VTGSAGWGPEPLPYSAFAGGASAPRCRRNGGTCVLGSCFVCPAHFTGRVCEHDQRR 120

DB 67 VTGSAGWGPEPLPYSAFAGGASAPRCRRNGGTCVLGSCFVCPAHFTGRVCEHDQRR 126

QY 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSGAGAPSLLL 180

DB 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSGAGAPSLLL 186

QY 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGLGHRL 223

DB 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGLGHRL 229

RESULT 7

ABP66887

ID ABP66887 standard; protein; 229 AA.

XX ABP66887;

AC ABP66887;

XX 09-DEC-2002 (first entry)

XX Human polypeptide SEQ ID NO 608.

DE

XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antispasmodic; antianemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX US2002090672-A1.
XX
XX 11-JUL-2002.
XX
XX 17-JAN-2001; 2001US-00764853.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 28-JUN-2000; 2000US-0214886P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 14-JUL-2000; 2000US-0217436P.
XX 14-JUL-2000; 2000US-0218280P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 22-AUG-2000; 2000US-0225758P.
XX 22-AUG-2000; 2000US-0226668P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 03-SEP-2000; 2000US-0229349P.
XX 03-SEP-2000; 2000US-0229513P.
XX 08-SEP-2000; 2000US-0231413P.
XX 21-SEP-2000; 2000US-0234223P.
XX 21-SEP-2000; 2000US-0234274P.
XX 23-SEP-2000; 2000US-0234997P.
XX 27-SEP-2000; 2000US-0235834P.
XX 29-SEP-2000; 2000US-0236327P.
XX 29-SEP-2000; 2000US-0236367P.
XX 29-SEP-2000; 2000US-0236368P.
XX 29-SEP-2000; 2000US-0236389P.
XX 29-SEP-2000; 2000US-0236370P.
XX 02-OCT-2000; 2000US-0236802P.
XX 02-OCT-2000; 2000US-0237037P.
XX 02-OCT-2000; 2000US-0237038P.
XX 02-OCT-2000; 2000US-0237039P.
XX 02-OCT-2000; 2000US-0237040P.
XX 13-OCT-2000; 2000US-0239935P.
XX 20-OCT-2000; 2000US-0240960P.
XX 20-OCT-2000; 2000US-0241785P.
XX 20-OCT-2000; 2000US-0241809P.
XX 01-NOV-2000; 2000US-0244617P.
XX 17-NOV-2000; 2000US-0249299P.
XX 08-DEC-2000; 2000US-0251856P.
XX 08-DEC-2000; 2000US-0251868P.
XX 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;

XX WPI; 2002-681727/73.
DR N-PSDB; ABV83859.
XX
XX Novel polypeptide useful for diagnosis, prognosis, prevention, and
PT treatment of immune, hyperproliferative, renal, respiratory,
PT cardiovascular, reproductive, endocrine, gastrointestinal and
PT neurological disorders.
XX
PS Claim 11; SEQ ID NO 608; 369pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABV83682-ABV84101) and proteins
CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 229 AA;

Query Match 100.0%; Score 223; DB 5; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-195;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRHVRLLFTVSLALQIIINLGNYSQREKHNGRGEVTKVATQKHQSPINWTSHFGE 60
Db 7 MTRHVRLLFTVSLALQIIINLGNYSQREKHNGRGEVTKVATQKHQSPINWTSHFGE 66

Qy 61 VTGSAGWGPEEPLPYSRAPGEGASARPCRCNGGTCVLGSCVCPAHFTGRYCEHQR 120
Db 67 VTGSAGWGPEEPLPYSRAPGEGASARPCRCNGGTCVLGSCVCPAHFTGRYCEHQR 126

Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSL 180
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSL 186

Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGLGHL 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGLGHL 229

RESULT 8
AB890336
ID AB890336 standard; protein; 223 AA.
XX
AC AB890336;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2712.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
XX WO200190304-A2.
XX
XX 29-NOV-2001.

```
XX PF 18-MAY-2001; 2001WO-US016450.
XX XX
XX PR 19-MAY-2000; 2000US-0205515P.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Birse CE, Rosen CA;
XX XX
XX DR WPI; 2002-122018/16.
XX DR N-PSDB; ABL90745.
XX XX
XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
XX PT prevention of neural, immune system, muscular, reproductive,
XX PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
XX PT disorders.
XX PS
XX PS Claim 11; SEQ ID NO 2712; 2081pp + Sequence Listing; English.
XX XX
XX CC The invention relates to novel genes (ABL9449-ABL90853) and proteins
XX CC (ABB9040-ABB9044) useful for preventing, treating or ameliorating
XX CC medical conditions e.g. by protein or gene therapy. The genes are
XX CC isolated from a range of human tissues disclosed in the specification.
XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
XX CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX CC infectious diseases such as viral, bacterial, fungal and parasitic
XX CC infections. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 223 AA;
XX XX
XX Query Match 83.9%; Score 187; DB 5; Length 223;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-162;
XX Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 37 EVTKVATQKHRSQPLNWTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCRCNGGT 96
DB |||||||
DB 37 EVTKVATQKHRSQPLNWTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCRCNGGT 96
QY 97 CVLGSCFCVCPAHFTGRYCEHDDRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
DB |||||||
DB 97 CVLGSCFCVCPAHFTGRYCEHDDRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
QY 157 CDPKDFLASHAGPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216
DB |||||||
DB 157 CDPKDFLASHAGPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216
QY 217 PGLGHRLL 223
DB |||||||
DB 217 PGLGHRLL 223
XX XX
XX RESULT 9
XX ABUS6711
XX ID ABUS6711 standard; protein; 223 AA.
XX AC
XX AC ABUS6711;
XX XX
XX DT 02-APR-2003 (first entry)
XX XX
XX DE Lung cancer-associated polypeptide #304.
XX XX
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
```

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KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX XX
XX OS Unidentified.
XX OS
XX PN WO200286443-A2.
XX XX
XX PD 31-OCT-2002.
XX XX
XX PF 18-APR-2002; 2002WO-US012476.
XX XX
XX PR 18-APR-2001; 2001US-0284770P.
XX PR 10-MAY-2001; 2001US-0290492P.
XX PR 09-NOV-2001; 2001US-0339445P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 29-NOV-2001; 2001US-0334370P.
XX PR 12-APR-2002; 2002US-0372246P.
XX XX
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX XX
XX PI Aziz N, Murray R;
XX XX
XX DR WPI; 2003-093161/08.
XX DR N-PSDB; ABX76440.
XX XX
XX PT Detecting a lung cancer-associated transcript in a cell from a patient
XX PT for treating lung cancer, by contacting a biological sample from the
XX PT patient with a polynucleotide that exhibits increased or decreased
XX PT expression in lung cancer.
XX XX
XX PS Claim 27; Page 426; 453pp; English.
XX XX
XX CC The invention relates to a method for detecting a lung cancer-associated
XX CC transcript in a cell from a patient, comprising contacting a biological
XX CC sample from the patient with a polynucleotide that selectively hybridises
XX CC to a sequence that is at least 80 % identical to a gene that exhibits
XX CC increased or decreased expression in lung cancer samples. Lung cancer-
XX CC associated polynucleotides and polypeptides are used for identifying a
XX CC compound that modulates a lung cancer-associated polypeptide, for
XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung
XX CC cancer in a patient and for treating a mammal having lung cancer by
XX CC administering a modulatory compound identified. The methods are useful
XX CC for treating lung cancer, such as small cell lung cancer, non-small cell
XX CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX CC for diagnostic purposes and as targets for screening for therapeutic
XX CC compounds that modulate lung cancer, such as antibodies. Sequences
XX CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
XX CC invention
XX XX
XX SQ Sequence 223 AA;
XX XX
XX Query Match 83.9%; Score 187; DB 6; Length 223;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-162;
XX Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 37 EVTKVATQKHRSQPLNWTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCRCNGGT 96
DB |||||||
DB 37 EVTKVATQKHRSQPLNWTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCRCNGGT 96
QY 97 CVLGSCFCVCPAHFTGRYCEHDDRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
DB |||||||
DB 97 CVLGSCFCVCPAHFTGRYCEHDDRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
QY 157 CDPKDFLASHAGPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216
DB |||||||
DB 157 CDPKDFLASHAGPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216
QY 217 PGLGHRLL 223
DB |||||||
DB 217 PGLGHRLL 223
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CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
XX SQ Sequence 223 AA;
    Query Match      83.9%; Score 187; DB 7; Length 223;
    Best Local Similarity 100.0%; Pred. No. 1.3e-162;
    Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 EVTKVATQKQRQSPNLTSSHFGEVTSAGWGPEEPPLPYSAFGEASARPCRCRNGGT 96
Db 37 EVTKVATQKQRQSPNLTSSHFGEVTSAGWGPEEPPLPYSAFGEASARPCRCRNGGT 96

Qy 97 CVLGSFVCVPAHFTGRYCEHDQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Db 97 CVLGSFVCVPAHFTGRYCEHDQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

Qy 157 CDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLLRPDAPAHPRSLVPSVLQRRRRPCGR 216
Db 157 CDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLLRPDAPAHPRSLVPSVLQRRRRPCGR 216

Qy 217 PGLGHRL 223
Db 217 PGLGHRL 223

RESULT 11
ADN39975
ID ADN39975 standard; protein; 223 AA.
XX
AC ADN39975;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C345.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulneryary; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX WO2003042661-A2.
XX
XX PD 22-MAY-2003.
XX
XX PF 13-NOV-2002; 2002WO-US036810.
XX
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 21-NOV-2001; 2001US-0332464P.
XX PR 29-NOV-2001; 2001US-0334393P.
XX PR 03-DEC-2001; 2001US-0335394P.
XX PR 14-DEC-2001; 2001US-0340376P.
XX PR 08-JAN-2002; 2002US-0347211P.
XX PR 10-JAN-2002; 2002US-0347349P.
XX PR 08-FEB-2002; 2002US-035250P.
XX PR 13-FEB-2002; 2002US-0356714P.
XX PR 20-FEB-2002; 2002US-0359077P.
XX PR 29-MAR-2002; 2002US-0368809P.
XX PR 04-APR-2002; 2002US-0370110P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PR 05-JUN-2002; 2002US-0386614P.
XX PR 16-JUL-2002; 2002US-0396839P.
XX PR 22-JUL-2002; 2002US-0397775P.
XX PR 22-JUL-2002; 2002US-0397845P.
XX PR 09-SEP-2002; 2002US-0409450P.
XX
XX (BOSB-) BOS BIOTECHNOLOGY INC.
XX
XX PA Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI; 2003-468649/44.
XX
XX DR N-PSDB; ADN39103.
XX
XX PT Determining the presence or absence of a pathological cell in a patient,
XX PT useful for diagnosing, prognosing or treating cancer, comprises detecting
XX PT a nucleic acid in a biological sample.
XX
XX PS Claim 12; SEQ ID NO 422; 1385pp; English.
XX
XX CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX CC whose expression is upregulated or downregulated in specific cancers or
XX CC other diseases such as angiogenic or fibrotic disorders, and to methods
XX CC of determining the presence or absence of a pathological cell in a
XX CC patient by detecting a nucleic acid at least 80% identical to those of
XX CC the invention or by detecting a polypeptide of the invention. The
XX CC invention also relates to expression vectors and host cells comprising a
XX CC nucleic acid of the invention; antibodies which specifically bind a
XX CC polypeptide of the invention; use of such antibodies for drug targeting;
XX CC and methods of screening for modulators of activity or expression of the
XX CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX CC antibodies and methods are useful for diagnosing, prognosing and treating
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XX (BOSB-) EOS BIOTECHNOLOGY INC.

PI Afar D, Aziz N, Gineburg WM, Gish KC, Glynn R, Hevezi PA;

PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX WPI; 2003-458649/44.

DR N-PSDB; ADN39758.

XX Determining the presence or absence of a pathological cell in a patient,

PT useful for diagnosing, prognosing or treating cancer, comprises detecting

PT a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO C345; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

CC whose expression is upregulated or downregulated in specific cancers or

CC other diseases such as angiogenic or fibrotic disorders, and to methods

CC of determining the presence or absence of a pathological cell in a

CC patient by detecting a nucleic acid at least 80% identical to those of

CC the invention or by detecting a polypeptide of the invention. The

CC invention also relates to expression vectors and host cells comprising a

CC nucleic acid of the invention; antibodies which specifically bind a

CC polypeptide of the invention; use of such antibodies for drug targeting;

CC and methods of screening for modulators of activity or expression of the

CC polypeptides and nucleic acids. The nucleic acids, polypeptides,

CC antibodies and methods are useful for diagnosing, prognosing and treating

CC cancer and other conditions such as psoriasis, ischaemia, heart disease,

CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC neovascularisation syndromes, scarring and uterine fibroids. They may

CC also be useful in wound healing and in contraception. The present

CC sequence represents a polypeptide of the invention.

XX

SQ Sequence 223 AA;

Query Match 83.9%; Score 187; DB 7; Length 223;

Best Local Similarity 100.0%; Pred. No. 1.3e-162; Indels 0; Gaps 0;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 EVTKVATQKHKRQSPNLTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCCRNGGT 96

DB 37 EVTKVATQKHKRQSPNLTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCCRNGGT 96

QY 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

DB 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

QY 157 CDPKDFLASHAGPSAGGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216

DB 157 CDPKDFLASHAGPSAGGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216

QY 217 PGLGHRLL 223

DB 217 PGLGHRLL 223

RESULT 12

ID ADY85963

XX ADY85963 standard; protein; 223 AA.

AC ADY85963;

XX

XX 16-JUN-2005 (first entry)

XX Human Criptic protein, a member of the EGF-CFC family Seq 4.

XX cell signaling; oncogenesis; antisense therapy; cytostatic; mutagenesis;

XX protein interaction; oncoprotein.

XX Homo sapiens.

XX W02005028433-A2.

XX

PD 31-MAR-2005.

XX

PF 14-SEP-2004; 2004WO-US029967.

XX

PR 15-SEP-2003; 2003US-0503046P.

XX

PA (RERE-) RES DEV FOUND.

XX

PI Vale W, Gray PC, Harrison CA;

XX WPI; 2005-242562/25.

DR

XX Augmenting signaling of a ligand of receptor serine kinase in a cell

PT comprises inhibiting the formation of complexes between Cripto and the

PT ligand on the surface of the cell.

XX

PS Disclosure; SEQ ID NO 4; 60pp; English.

XX

CC This invention relates to a novel method for augmenting signaling of a

CC ligand of a receptor serine kinase within a cell by inhibiting the

CC formation of complexes between Cripto and this ligand on the surface of

CC the cell. Specifically, it refers to TGF-beta and activin which are the

CC ligands of serine kinase receptors and which regulate tissue homeostasis

CC by activating the Smad2/3 intracellular signaling pathway; disruption of

CC this signaling pathway is associated with oncogenesis and tumorigenesis.

CC As such, the present invention describes a method for augmenting Smad2/3

CC signaling in a cell by administering a mutant ligand that retains

CC signaling activity but is unable to bind to Cripto, and thus bypasses

CC antagonism by Cripto. Note that augmentation of signaling increases

CC phosphorylation and activation of Smad2 and Smad3 in the cell, such that

CC it decreases the proliferative rate of the cell. The receptor serine

CC kinase is a type I activin receptor-like kinases-4 or -5 (ALK-4 or ALK-5)

CC and the formation of complexes is inhibited by suppressing expression of

CC Cripto using antisense oligonucleotides (siRNA) directed against Cripto,

CC and also mutating at least one allele of Cripto by homologous

CC recombination. Accordingly, pharmaceutical compositions derived thereof

CC exhibit cytostatic activity. This polypeptide sequence is the human

CC Criptic protein, a member of the EGF-CFC (Epidermal Growth Factor-Cripto,

CC FRL-1, Criptic) family of proteins of the invention.

XX

SQ Sequence 223 AA;

Query Match 83.9%; Score 187; DB 9; Length 223;

Best Local Similarity 100.0%; Pred. No. 1.3e-162; Indels 0; Gaps 0;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 EVTKVATQKHKRQSPNLTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCCRNGGT 96

DB 37 EVTKVATQKHKRQSPNLTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCCRNGGT 96

QY 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

DB 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

QY 157 CDPKDFLASHAGPSAGGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216

DB 157 CDPKDFLASHAGPSAGGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216

QY 217 PGLGHRLL 223

DB 217 PGLGHRLL 223

RESULT 13

ID AAU16957

XX AAU16957 standard; protein; 231 AA.

XX

XX AAU16957;

XX

XX 07-NOV-2001 (first entry)

XX Human novel secreted protein, SEQ ID 198.

XX

PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476222/51.
DR N-PSDB; AAS26862.
XX
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT hemophilia.
XX
XX Claim 11; SEQ ID NO 198; 601bp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence represents a novel secreted protein of the invention. Note: The
Query Match 83.9%; Score 187; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.3e-162; Mismatches 0; Indels 0; Gaps 0;
Matches 187; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
Qy 37 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLYSRAFGEGASARPCCRNGGT 96
Db 45 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLYSRAFGEGASARPCCRNGGT 104
Qy 97 CVLGSEFCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Db 105 CVLGSEFCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 164
Qy 157 CDPKDFLASHAHGSPSAGGAPSLLLLPALLHLLRPDPAHPRSLVPSVLQRRPCGR 216
Db 165 CDPKDFLASHAHGSPSAGGAPSLLLLPALLHLLRPDPAHPRSLVPSVLQRRPCGR 224
Qy 217 PGLGHRL 223
Db 225 PGLGHRL 231
RESULT 14
AAW09111
ID AAW09111 standard; protein; 230 AA.
XX
XX
AC AAW09111;

XX 16-APR-1997 (first entry)
XX Human criptin growth factor.
DE
XX
XX Criptin growth factor; CGF; angiogenesis; wound healing; vulvurary;
KW muscle wastage; osteoporosis; implant fixation; tissue regeneration;
KW pancreas cancer; diagnosis; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide
XX
PN W09639420-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1995; 95WO-US007087.
XX
XX 05-JUN-1995; 95WO-US007087.
PR (HUMA-) HUMAN GENOME SCI INC.
XX
XX Meissner PS, Coleman TA;
PI
XX
DR WPI; 1997-043055/04.
DR N-PSDB; AAT51058.
XX
XX New isolated human Criptin Growth Factor polypeptide - which can be used
PT to stimulate angiogenesis and develop products for use in diagnosis and
PT therapy.
XX
XX Claim 12; Fig 1; 52pp; English.
XX
XX Human criptin growth factor (CGF) (AAW09111) is a novel polypeptide
CC structurally related to human cripto growth factor. It is overexpressed
CC and secreted by certain types of cancer cells, e.g. pancreatic cancers.
CC Recombinant CGF can be produced in host cells utilising vectors
CC incorporating a CGF cDNA clone (AAT51058) isolated from a human
CC pancreatic cancer tissue cDNA library. CGF can be used to treat e.g.
CC muscle wasting diseases, osteoporosis, to aid implant fixation, to
CC stimulate tissue regeneration and wound healing, to promote angiogenesis
CC and to stimulate proliferation of vascular smooth muscle and endothelial
CC cell prodn. It can also be used as a marker for cancer diagnosis
XX
SQ Sequence 230 AA;
Query Match 66.8%; Score 149; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 8.1e-128; Mismatches 0; Indels 0; Gaps 0;
Matches 149; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
Qy 37 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLYSRAFGEGASARPCCRNGGT 96
Db 37 EVTKVATQKHRSQPLNWTSSHFGEVGTGSAEGWGPEEPPLYSRAFGEGASARPCCRNGGT 96
Qy 97 CVLGSEFCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Db 97 CVLGSEFCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Qy 157 CDPKDFLASHAHGSPSAGGAPSLLLLPALLHLLRPDPAHPRSLVPSVLQRRPCGR 185
Db 157 CDPKDFLASHAHGSPSAGGAPSLLLLPALLHLLRPDPAHPRSLVPSVLQRRPCGR 185
RESULT 15
AAG77914
ID AAG77914 standard; protein; 223 AA.
XX
XX AAG77914;
XX
XX 23-JAN-2002 (first entry)
DT

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 18:52:05 ; Search time 297 Seconds
(without alignment)
694.540 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTRWHVRLFTVSLALQII.....PSVLQRRRRCGRGLGHL 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 6

Total number of hits satisfying chosen parameters: 11635

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	187	83.9	223	1	CFC1_HUMAN
2	15.	6.7	202	1	P97766 mus musculus
3	14	6.3	191	2	Q2UZ56 XENLA
4	14	6.3	191	2	Q2VU96 XENLA
5	11	4.9	179	2	Q2VU94 XENLA
6	11	4.9	251	2	Q2UZ94 XENLA
7	11	4.9	251	2	Q2VU93 XENLA
8	8	3.6	105	2	Q53M57 ORYZA
9	8	3.6	105	2	Q60E85 ORYZA
10	8	3.6	158	2	Q5R283 DROSE
11	8	3.6	158	2	Q5R293 DROSI
12	8	3.6	158	2	Q9V901 DROME
13	8	3.6	346	2	Q5WB00 BACSK
14	8	3.6	353	2	Q5F349 CHICK
15	8	3.6	357	2	Q3P026 SGMM
16	8	3.6	375	2	Q4RMC1 TETNG
17	8	3.6	382	2	Q7QV27 GIALA
18	8	3.6	384	2	Q37YV8 SPHAR
19	8	3.6	409	2	Q43ZW8 SOLUS
20	8	3.6	415	2	Q4B045 BURK
21	8	3.6	456	1	GUNA_MIBI
22	8	3.6	655	2	Q8ST54 ENCCU
23	8	3.6	701	2	Q41C80 9BACI
24	8	3.6	721	2	Q7XQ88 ORYZA
25	8	3.6	752	2	Q42374 BRARE
26	8	3.6	762	2	Q4RS94 TETNG
27	8	3.6	793	2	Q13876 HUMAN
28	8	3.6	823	2	Q6X220 BOVINE
29	8	3.6	859	1	OBP_BHVIC
30	8	3.6	924	2	Q4DT24 TRYCR
31	8	3.6	927	2	Q4E329 TRYCR

32	8	3.6	1046	2	Q4S1V9 TETNG	Q4S1V9 tetraodon n
33	8	3.6	1085	2	Q3FR67 BURK	Q3FR67 rhodofexax
34	8	3.6	1152	2	Q4J8A9 SULAC	Q4J8A9 sulfolobus
35	8	3.6	1230	1	RPOM_HUMAN	O0411 homo sapien
36	8	3.6	1230	2	Q4G0F4 HUMAN	Q4G0F4 homo sapien
37	8	3.6	1324	2	Q4RJ05 TETNG	Q4RJ05 tetraodon n
38	8	3.6	1945	2	Q4RQ96 TETNG	Q4RQ96 tetraodon n
39	8	3.6	2030	2	Q4RHF2 TETNG	Q4RHF2 tetraodon n
40	8	3.6	2061	2	Q4SRM9 TETNG	Q4SRM9 tetraodon n
41	8	3.6	2468	2	Q800E4 BRARE	Q800E4 brachydanio
42	8	3.6	2524	1	NOTCH_XENLA	P21783 xenopus lae
43	8	3.6	2819	2	Q6W4W6 CHICK	Q6W4W6 gallus gall
44	8	3.6	2982	2	Q4RXP0 TETNG	Q4RXP0 tetraodon n
45	7	3.1	24	2	Q6LDJ0_HUMAN	Q6LDJ0 homo sapien

ALIGNMENTS

RESULT 1
CFC1_HUMAN
ID CFC1_HUMAN STANDARD; PRT; 223 AA.
AC Q9GZR3; Q53T05;
DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 07-MAR-2006, entry version 32.
DE Cryptic protein precursor.
GN Name=CFC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP CYS-112, CHARACTERIZATION OF VARIANT HTX2 CYS-112, AND VARIANTS TRP-78 AND CYS-189.
RX MEDLINE=20517351; PubMed=1062482; DOI=10.1038/81695;
RA Bamford R.N., Roessler E., Burdine R.D., Saplakoglu U., dela Cruz J., Splitt M., Towbin J., Bowers P., Marino B., Schier A.F., Shen M.M., Muenke M., Casey B.;
RA "Loss-of-function mutations in the EGF-CFC gene CFC1 are associated with human left-right laterality defects."; Nat. Genet. 26:365-369(2000).
RL [2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA], AND VARIANT TRP-78.
RP PubMed=15815621; DOI=10.1038/nature03466;
RX Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pepin K.H., Minx P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M., Becker M.C., Powell G.A., Delehaanty K.D., Miner T.L., Nash W.B., Krentzki C., Oddi L., Du H., Sun H., Bradshaw-Cordum H., Ali J., Carter J., Cordes M., Harris A., Isak A., van Brunt A., Nguyen C., Du F., Courtney L., Kalicki J., Ozersky P., Abbott S., Armstrong J., Belter E.A., Caruso L., Cedroni M., Cotton M., Davidson T., Desai A., Elliott G., Erb T., Fronick C., Gaige T., Haakenson W., Haglund K., Holmes A., Harkins R., Kim K., Kruchowski S.S., Strong C.M., Grewal N., Goyea E., Hou S., Levy A., Martinka S., Mead K., McEllean M.B., Meyer R., Randall-Maher J., Tomlinson C., Dauphin-Kohlberg S., Kozlowski-Reilly A., Shah N., Swearengen-Shahid S., Snider J., Strong J.T., Thompson J., Yoakum M., Leonard S., Pearson C., Trani L., Radionenko M., Waligorski J.E., Wang C., Rock S.M., Tin-Wollam A.-M., Maupin R., Latreille P., Wendt M.C., Yang S.-P., Pohl C., Wallis J.W., Spieth J., Bieri T.A., Berkowicz N., Nelson J.O., Osborne J., Ding L., Meyer R., Sabo A., Shatland Y., Sinha P., Wohlmann P.E., Cook L.L., Hickenbotham M.T., Eldred J., Williams D., Jones T.A., She X., Ciccirelli F.D., Izaurralde E., Taylor J., Schmutz J., Myers R.M., Cox D.R., Huang X., McPherson J.D., Mardis E.R., Clifton S.W., Warren W.C., Chinwalla A.T., Eddy S.R., Marra M.A., Ovcharenko I., Furey T.S., Miller W., Eichler E.E., Bork P., Suyama M., Torrents D., Waterston R.H., Wilson R.K.;
RT "Generation and annotation of the DNA sequences of human chromosomes 2 and 4.";

RL Nature 434:724-731(2005).
 RN [3]
 RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.J., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaly S.J.,
 RA Boak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzowski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP VARIANT TRP-78, AND INVOLVEMENT IN DTGA AND CTHM.
 RX PubMed=11799476;
 RA Goldmuntz E., Bamford R., Karkera J.D., dela Cruz J., Roessler E.,
 RA Muenke M.;
 RT "CFCL mutations in patients with transposition of the great arteries
 and double-outlet right ventricle.";
 RL Am. J. Hum. Genet. 70:776-780(2002).
 CC -I- FUNCTION: Involved in the correct establishment of the left-right
 axis. May play a role in mesoderm and/or neural patterning during
 gastrulation.
 CC -I- PTH: N-glycosylated (By similarity).
 CC -I- DISEASE: Defects in CFCL are a cause of visceral heterotaxy (HTX2)
 [MIM:605376]. HTX2 is an autosomal form of visceral heterotaxy
 (HTX). HTX is characterized by a variable group of congenital
 anomalies that include complex cardiac malformations and situs
 inversus or situs ambiguus.
 CC -I- DISEASE: Defects in CFCL are a cause of transposition of the great
 arteries, dextro-looped (DTGA) [MIM:608808]. The more common form
 of DTGA, consists of complete inversion of the great vessels, so
 that the aorta incorrectly arises from the right ventricle and the
 pulmonary artery incorrectly arises from the left ventricle. This
 creates completely separate pulmonary and systemic circulatory
 systems, an arrangement that is incompatible with life. Patients
 often have atrial and/or ventricular septal defects or other types
 of shunting that allow some mixing between the circulations in
 order to support life minimally, but surgical intervention is
 always required.
 CC -I- DISEASE: Defects in CFCL are a cause of conotruncal heart
 malformations (CTHM) [MIM:217095]. CTHM consist of cardiac outflow
 tract defects, such as tetralogy of Fallot, pulmonary atresia,
 double-outlet right ventricle, truncus arteriosus communis, and
 aortic arch anomalies.
 CC -I- SIMILARITY: Contains 1 EGF-like domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC ENBL; AF312769; AAG30294.1; -; mRNA.
 CC ENBL; AF312925; AAG42475.1; -; Genomic DNA.
 CC ENBL; AC013269; AAY14955.1; -; Genomic DNA.
 CC ENBL; BC069508; AHH69508.1; -; mRNA.
 CC ENBL; BC074825; AAH74825.1; -; mRNA.
 CC ENBL; BC074826; AAH74826.1; -; mRNA.
 CC ENBL; BC110080; AAI10081.1; -; mRNA.
 CC HSSP; P00750; 1TPG.
 CC HGNC; HGNC:18292; CFCL.
 CC MIM; 217095; phenotype.

DR MIM; 605194; gene.
 DR MIM; 605376; phenotype.
 DR MIM; 608808; P:determination of left/right symmetry; NAS.
 DR GO; GO:0007368; P:determination of left/right symmetry; NAS.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR Pfam; PF00008; EGF; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 KW Developmental protein; Disease mutation; EGF-like domain;
 KW Gastrulation; Glycoprotein; Polymorphism; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 223 Cytic protein.
 FT DOMAIN 86 115 EGF-like.
 FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).
 FT DISULFID 90 97 By similarity.
 FT DISULFID 91 103 By similarity.
 FT DISULFID 105 114 By similarity.
 FT VARIANT 78 78 R -> W (in dbSNP:2579433).
 FT VARIANT 112 112 R -> C (in HTX2; complete loss of
 activity; abnormal cell surface
 localization).
 FT VARIANT 189 189 R -> C.
 FT SEQUENCE 223 AA; 24612 MW; B52852A0ABCFA3 CRC64;
 Query Match 83.9%; Score 187; DB 1; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1.2e-172;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 EVTKVATQKHROSPLNWTSSHFGEVTSAGWGPEPLPYSRAFGSGASAPRCRCNGGT 96
 DB 37 EVTKVATQKHROSPLNWTSSHFGEVTSAGWGPEPLPYSRAFGSGASAPRCRCNGGT 96
 QY 97 CVLGSCFCVCPAIFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLOTDR 156
 DB 97 CVLGSCFCVCPAIFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLOTDR 156
 QY 157 CDPKDFLASHAGPSAGGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216
 DB 157 CDPKDFLASHAGPSAGGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216
 QY 217 PGLGHRLL 223
 DB 217 PGLGHRLL 223
 RESULT 2
 CFCL MOUSE STANDARD; PRT; 202 AA.
 ID CFCL MOUSE
 AC P97766; Q496U5; Q9JIB7;
 DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1997, sequence version 1.
 DT 07-MAR-2006, entry version 30.
 DE Cryptic protein precursor.
 GN Name=Cfcl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA], FUNCTION, TISSUE SPECIFICITY,
 RP DEVELOPMENTAL STAGE, AND GLYCOSYLATION.
 RC STRAIN=129/SV;
 RX MEDLINE=97178978; PubMed=9053319;
 RA Shen M.M., Wang H., Leder P.;
 RT "A differential display strategy identifies Cryptic, a novel EGF-

related gene expressed in the axial and lateral mesoderm during mouse gastrulation."

Development 124:429-442(1997).

[2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. DOI=10.1073/pnas.2426038999;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Cernichio P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3]

NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-154.
RA MEDLINE=20480687; PubMed=11024280; DOI=10.1016/S0378-1119(00)00337-1;
RX Colas J.-F., Schoenwolf G.C.;
RT "Subtractive hybridization identifies chick-cripto, a novel EGF-CFC
RT ortholog expressed during gastrulation, neurulation and early
RT cardiogenesis."

Gene 255:203-217(2000).

[4]

FUNCTION, AND KNOCK-OUT.
RX MEDLINE=20045034; PubMed=10574770; DOI=10.1016/S0960-9822(00)80059-7;
RA Gaio U., Schweickert A., Fischer A., Garratt A.N., Mueller T.,
RA Oszcelik C., Lankes W., Strehle M., Britsch S., Blum M.,
RA Birmelmeier C.;
RT "A role of the cryptic gene in the correct establishment of the left-
RT right axis."

Curr. Biol. 9:1339-1342(1999).

-1- FUNCTION: Involved in the correct establishment of the left-right
axis. May play a role in mesoderm and/or neural patterning during
gastrulation.

-1- TISSUE SPECIFICITY: No expressed in adult tissues.

-1- DEVELOPMENTAL STAGE: Expressed during gastrulation (from 6.5 dpc
to 11 dpc) in two spatial domains that correspond to the axial and
lateral mesoderm. In the first domain expression is progressively
localized to the anterior primitive streak, the head process, and
the node and notochordal. In the second domain, expression is
initially concentrated in the lateral region of the egg cylinder,
and is later found circumferentially in the intermediate and
lateral plate mesoderm. Furthermore, the expression can also be
detected at the early head-fold stage in the midline
neuroectoderm, and consequently is an early marker for the
prospective floor plate of the neural tube. Expression ceases at
the end of gastrulation, and has not been observed in later
embryonic stages.

-1- PTM: N-glycosylated.

-1- MISCELLANEOUS: Mice lacking functional Cfc1 showed positional
defects in internal organs. The lung presents a right pulmonary
isomerism. The stomach is located on either the left or the right
and the spleen is small and has an abnormal shape. The apex of the
heart pointed to the right or left. In addition malpositioning of
heart outflow tracts is observed, the aorta is connected to the
right ventricle and emerged from the heart in a ventral position
and to the right of the pulmonary artery. This one is connected to
either the left or the right ventricle.

-1- SIMILARITY: Contains 1 EGF-like domain.

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CC EMBL; U57720; AAC53042.1; -; mRNA.
CC EMBL; BC100705; AA100706.1; -; mRNA.
CC EMBL; BC100706; AA100707.1; -; mRNA.
CC EMBL; BC100708; AA100709.1; -; mRNA.
CC EMBL; BC100711; AA100712.1; -; mRNA.
CC EMBL; AF242430; AAF76323.1; -; Genomic_DNA.
CC HSPB; P00749; IURK.
CC Ensembl; ENSMUSG00000026124; Mus musculus.
CC MGI; MGI:109448; Cccl.
CC GO; GO:0005615; C:extracellular space; TAS.
CC InterPro; IPR000742; EGF_3.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR013032; EGF_like_reg.
CC Pfam; PF00008; EGF_1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PSS0026; EGF_3; 1.
CC Developmental protein; EGF-like domain; Gastrulation; Glycoprotein;
KW Signal.
FT SIGNAL 1 35 Potential.
FT CHAIN 36 202 Cryptic protein.
FT DOMAIN 94 123 EGF-like.
FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
FT DISULFID 98 105 By similarity.
FT DISULFID 99 111 By similarity.
FT DISULFID 113 122 By similarity.
FT CONFLICT 83 83 P -> T (in Ref. 2; AA100707).
SQ SEQUENCE 202 AA; 21792 MW; 57035AD339A16FD7 CRC64;

Query Match 6.7%; Score 15; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 NGGTCVLGSGFCVCPA 107
DB 101 NGGTCVLGSGFCVCPA 115
|||||

RESULT 3
QZU296 XENLA PRELIMINARY; PRT; 191 AA.
AC QZU296; 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Crip2-2.
GN Name=C2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Mesobatrachia; Pipidae;
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dorey K., Hill C.S.;
RT "Role of EGF-CFC family members in Nodal signalling during early
RT xenopus development."
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AJ864899; CA115753.1; -; mRNA.
SQ SEQUENCE 191 AA; 21651 MW; D4E992122C89495D CRC64;

Query Match 6.3%; Score 14; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 NGGTCVLGSGFCVCP 106

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Db          93 NGGTCVLGSGFCVCP 106
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RESULT 4
Q2VU96_XENLA PRELIMINARY; PRT; 191 AA.
AC Q2VU96;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE CR2.
GN Names=CR2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
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CC -----
DR EMBL; AY796186; AAX81598.1; -; mRNA.
SQ SEQUENCE 191 AA; 21681 MW; 95E9920E40F95531 CRC64;

Query Match      6.3%; Score 14; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 88-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFCVCP 106
|||||
Db          93 NGGTCVLGSGFCVCP 106
|||||
RESULT 5
Q2VU94_XENLA PRELIMINARY; PRT; 179 AA.
AC Q2VU94;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE CR3 short transcript variant (Cripto-3 short).
GN Names=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
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CC -----
DR EMBL; AY796186; AAX81598.1; -; mRNA.
SQ SEQUENCE 191 AA; 21681 MW; 95E9920E40F95531 CRC64;

Query Match      6.3%; Score 14; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 88-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFCVCP 106
|||||
Db          93 NGGTCVLGSGFCVCP 106
|||||
RESULT 6
Q2VU94_XENLA PRELIMINARY; PRT; 251 AA.
AC Q2VU94;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Cripto-3 long.
GN Names=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Dorey K., Hill C.S.;
RT "Role of EGF-CFC family members in Nodal signalling during early
RT Xenopus development.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ864901; CAI15755.1; -; mRNA.
SQ SEQUENCE 251 AA; 27813 MW; D0256376A829A37E CRC64;

Query Match      4.9%; Score 11; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFC 103
|||||
Db          152 NGGTCVLGSGFC 162
|||||
RESULT 7
Q2VU93_XENLA PRELIMINARY; PRT; 251 AA.
AC Q2VU93;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE CR3 long transcript variant.
GN Names=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Tissue=Embryo stage 10.5;
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
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CC -----
DR EMBL; AY796186; AAX81598.1; -; mRNA.
SQ SEQUENCE 251 AA; 27813 MW; D0256376A829A37E CRC64;

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DR EMBL; AJ864900; CAI15754.1; -; mRNA.
KW EGF-like domain; Repeat.
SQ SEQUENCE 179 AA; 20060 MW; 912E723BE597D6CE CRC64;

Query Match      4.9%; Score 11; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFC 103
|||||
Db          80 NGGTCVLGSGFC 90
|||||
RESULT 6
Q2VU94_XENLA PRELIMINARY; PRT; 251 AA.
AC Q2VU94;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Cripto-3 long.
GN Names=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Dorey K., Hill C.S.;
RT "Role of EGF-CFC family members in Nodal signalling during early
RT Xenopus development.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ864901; CAI15755.1; -; mRNA.
SQ SEQUENCE 251 AA; 27813 MW; D0256376A829A37E CRC64;

Query Match      4.9%; Score 11; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFC 103
|||||
Db          152 NGGTCVLGSGFC 162
|||||
RESULT 7
Q2VU93_XENLA PRELIMINARY; PRT; 251 AA.
AC Q2VU93;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE CR3 long transcript variant.
GN Names=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Tissue=Embryo stage 10.5;
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
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CC -----
DR EMBL; AY796186; AAX81598.1; -; mRNA.
SQ SEQUENCE 251 AA; 27813 MW; D0256376A829A37E CRC64;

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CC -----
DR EMBL: AY796189; AAX81599.1; -; mRNA.
KW EGF-like domain, Repeat.
SQ SEQUENCE 251 AA; 27849 MW; DODFCC140A3E0BFE CRC64;

Query Match 4.9%; Score 11; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 NGGTCVLGSFC 103
Db 152 NGGTCVLGSFC 162

RESULT 8
Q53M57 ORYSA PRELIMINARY; PRT; 105 AA.
AC Q53M57;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Expressed protein.
GN ORFNames=LOC Os11g14190;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,
RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Tsitrin T.,
RA Bera J., Kim M., Jin S., Fadrosch D., Vuong H., Overton II L.,
RA Reardon M., Weaver B., Johri S., Lewis M., Utterback T., Van Aken S.,
RA Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Tobst S.,
RA de Vazeilles A., White O., Salzberg S., Fraser C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AC137824; AAX96767.1; -; Genomic DNA.
DR EMBL: DP000010; AB92348.1; -; Genomic DNA.
SQ SEQUENCE 105 AA; 11604 MW; 91390CAC01836B7C CRC64;

Query Match 3.6%; Score 8; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLLLLLP 183
Db 73 PSLLLLLP 80

RESULT 9
Q60B65 ORYSA PRELIMINARY; PRT; 105 AA.
AC Q60B65;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein OSJNBa0073E05.11.
GN Name=OSJNBa0073E05.11;

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OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OSJNBa0073E05 genomic sequence.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AC136219; AAV31337.1; -; Genomic DNA.
DR Gramene; Q60B65; -;
KW Hypothetical protein.
SQ SEQUENCE 105 AA; 10289 MW; 48FF3E18C287B182 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLLLLLP 183
Db 42 PSLLLLLP 49

RESULT 10
Q5R263 DROSE PRELIMINARY; PRT; 158 AA.
ID Q5R263;
AC Q5R263;
DT 04-JAN-2005, integrated into UniProtKB/TrEMBL.
DT 04-JAN-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE CG13869.
GN ORFNames=CG13869;
OS Drosophila sechellia (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15729003; DOI=10.1266/ggs.79.351;
RA Kawahara Y., Mateno T., Nozawa M., Shin-I T., Kohara Y., Aigaki T.;
RT "Comparative sequence analysis of a gene-dense region among closely
RT related species of Drosophila melanogaster.";
RL Genes Genet. Syst. 79:351-359 (2004).
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CC -----
DR EMBL: AB162351; BAD72913.1; -; Genomic DNA.
DR FlyBase; FBgn0082773; Dsec/CG13869.
DR InterPro; IPR006631; DUF_DM4_12.
DR Pfam; PF07841; DM4_12; 1.
DR SMART; SM00718; DM4_12; 1.
SQ SEQUENCE 158 AA; 18628 MW; 752363888A7DDA2B CRC64;

Query Match 3.6%; Score 8; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 LLHRLLRP 193
Db 102 LLHRLLRP 109

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RESULT 11
QSR293 DROS1 PRELIMINARY; PRT; 158 AA.
AC QSR293;
DT 04-JAN-2005, integrated into UniProtKB/TrEMBL.
DT 04-JAN-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE CG13869.
GN ORFNames=CG13869;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP PubMed=15729003; DOI=10.1266/ggs.79.351;
RA Kawahara Y., Matsuo T., Nozawa M., Shin-I T., Kohara Y., Aigaki T.;
RT "Comparative sequence analysis of a gene-dense region among closely
RT related species of Drosophila melanogaster.";
RL Genes Genet. Syst. 79:351-359(2004).
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CC -----
DR EMBL; AB162349; BAD72895.1; -; Genomic_DNA.
DR FlyBase; FBgn0082752; Dsln\CG13869.
DR InterPro; IPR006631; DUF_DM4_12.
DR Pfam; PF07841; DM4_12; 1.
DR SMART; SM00718; DM4_12; 1.
SQ SEQUENCE 158 AA; 18589 MW; 4C39B3C6BB06CEB1 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 186 LLHRLRLP 193
Db 102 LLHRLRLP 109

RESULT 12
QSV901 DROME PRELIMINARY; PRT; 158 AA.
AC QSV901;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE CG13869-PA.
GN ORFNames=CG13869, Dmel CG13869;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stapleton M., Strong R.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RN Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RN Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AE003793; AAF57503.1; -; Genomic_DNA.
DR FlyBase; FBgn0034486; CG13869.
DR InterPro; IPR006631; DUF_DM4_12.
DR Pfam; PF07841; DM4_12; 1.
DR SMART; SM00718; DM4_12; 1.
SQ SEQUENCE 158 AA; 18591 MW; CC28B147B1046DB7 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 LLHRLRP 193
Db 102 LLHRLRP 109

RESULT 13
Q5WB00_BACSK PRELIMINARY; PRT; 346 AA.
AC Q5WB00;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN OrderedLocNames=ABC3929;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN 1
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

CC
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DR EMBL; AP006627; BAD66460.1; -; Genomic_DNA.
DR InterPro; IPR007820; Put_NH3_mOase.
DR Pfam; PF05145; AmoA; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 346 AA; 36837 MW; 8BECA0D42874806F CRC64;

Query Match 3.6%; Score 8; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LFTVSLAL 17
Db 51 LFTVSLAL 58

RESULT 14
Q5F349_CHICK PRELIMINARY; PRT; 353 AA.
AC Q5F349;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 13.
DE Hypothetical protein.
GN ORFNames=RCJMB04_34j1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
```

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RA Fiedler P., Kutter S., Blagodatki A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis";
RL Genome Biol. 6:R6-R6(2005).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
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DR EMBL; AJ851801; CAH65435.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Chk_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Receptor; Transferase.
SQ SEQUENCE 353 AA; 40217 MW; 8F045CB5096887F6 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 APSLLLLL 182
Db 17 APSLLLLL 24

RESULT 15
Q3P0Z6_9GAMM PRELIMINARY; PRT; 357 AA.
AC Q3P0Z6;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Secretion protein HlyD precursor.
GN ORFNames=SdenDRAFT_0315;
OS Shewanella denitrificans OS217.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=318161;
RN 1
RA NUCLEOTIDE SEQUENCE.
RP STRAIN=OS-217;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Shewanella
RT denitrificans OS-217.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN 2
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OS-217;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Shewanella denitrificans
RT OS-217.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
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DR EMBL; AAU01000015; EAN70114.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
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DR GO; GO:0015428; F: type I protein secretor activity; IEA.
 DR GO; GO:0009306; P: protein secretion; IEA.
 DR InterPro; IPR006143; HlyD.
 DR InterPro; IPR003997; RtxD_bac.
 DR PRINTS; PR01490; RTXTOXIND.
 DR TIGRFAMs; TIGR01730; RND_mfp; 1.
 KW Signal.

FT SIGNAL 1 28 Potential.

SQ SEQUENCE 357 AA; 39181 MW; BBB91C4A932116A3 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 LLLPCALL 187

Db 11 LLLPCALL 18

Search completed: September 22, 2006, 19:00:17
 Job time : 302 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	149	66.8	230	1	US-08-471-371-2	Sequence 2, Appli	
2	8	3.6	363	2	US-09-252-991A-18016	Sequence 18016, A	
3	8	3.6	2523	1	US-08-185-433-18	Sequence 18, Appli	
4	8	3.6	2523	1	US-08-899-232-3	Sequence 3, Appli	
5	8	3.6	2523	2	US-09-121-457-3	Sequence 3, Appli	
6	7	3.1	69	2	US-09-489-039A-9115	Sequence 9115, Ap	
7	7	3.1	70	2	US-09-621-976-5356	Sequence 5356, Ap	
8	7	3.1	88	2	US-09-621-976-3983	Sequence 3983, Ap	
9	7	3.1	103	2	US-09-621-976-5415	Sequence 5415, Ap	
10	7	3.1	106	2	US-09-149-476-341	Sequence 341, App	
11	7	3.1	107	2	US-09-461-325-484	Sequence 484, App	
12	7	3.1	107	2	US-10-012-542-484	Sequence 484, App	
13	7	3.1	107	2	US-10-115-123-484	Sequence 484, App	
14	7	3.1	111	2	US-09-248-796A-26807	Sequence 26807, A	
15	7	3.1	112	2	US-09-621-976-3926	Sequence 3926, Ap	
16	7	3.1	115	2	US-10-104-047-3840	Sequence 3840, Ap	
17	7	3.1	119	2	US-09-991-181-165	Sequence 165, App	
18	7	3.1	119	2	US-09-990-444-165	Sequence 165, App	
19	7	3.1	119	2	US-09-997-333-165	Sequence 165, App	
20	7	3.1	119	2	US-09-992-598-165	Sequence 165, App	
21	7	3.1	119	2	US-09-989-735-165	Sequence 165, App	
22	7	3.1	119	3	US-09-989-726-165	Sequence 165, App	
23	7	3.1	119	3	US-09-997-514-165	Sequence 165, App	
24	7	3.1	119	3	US-09-989-728-165	Sequence 165, App	
25	7	3.1	119	3	US-09-997-349-165	Sequence 165, App	
26	7	3.1	119	3	US-09-997-653-165	Sequence 165, App	

QY 97 CVLGSCVCPAHTGTRYCEHDQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
|
Db 97 CVLGSCVCPAHTGTRYCEHDQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
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QY 157 CDPKDFLASHAGPSAGGAPSLLLLPKA 185
|
Db 157 CDPKDFLASHAGPSAGGAPSLLLLPKA 185
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RESULT 2
US-09-252-991A-18016
; Sequence 18016, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18016
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18016
Query Match 3.6%; Score 8; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 GASARPRC 90
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Db 352 GASARPRC 359
|
RESULT 3
US-08-185-432-18
; Sequence 18, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Buseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mierock, S. Leslie
; REGISTRATION NUMBER: 19,872
; REFERENCE/DOCKET NUMBER: 7326-006

QY 91 CRNGGTCV 98
|
Db 265 CRNGGTCV 272
|
RESULT 4
US-08-899-232-3
; Sequence 3, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2523
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-08-899-232-3
Query Match 3.6%; Score 8; DB 2; Length 2523;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 CRNGGTCV 98
|
Db 265 CRNGGTCV 272
|
RESULT 5
US-09-121-457-3
; Sequence 3, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2523
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-09-121-457-3
Query Match 3.6%; Score 8; DB 2; Length 2523;
Best Local Similarity 100.0%; Pred. No. 85;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CRGGTCV 98
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Db 265 CRGGTCV 272

RESULT 6

US-09-489-039A-9115
; Sequence 9115, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9115
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9115

Query Match 3.1%; Score 7; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 APSLLLL 181
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Db 8 APSLLLL 14

RESULT 7

US-09-621-976-5356
; Sequence 5356, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5356
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17...-1
; NAME/KEY: UNSURE
; LOCATION: 39
; OTHER INFORMATION: Xaa = Ala,Pro
US-09-621-976-5356

Query Match 3.1%; Score 7; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 GGAPSL 179
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Db 60 GGAPSL 66

RESULT 8

US-09-621-976-3983

; Sequence 3983, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3983
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
US-09-621-976-3983

Query Match 3.1%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 APSLLLL 181
|||||||
Db 8 APSLLLL 14

RESULT 9

US-09-621-976-5415
; Sequence 5415, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5415
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
US-09-621-976-5415

Query Match 3.1%; Score 7; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 APSLLLL 181
|||||||
Db 8 APSLLLL 14

RESULT 10

US-09-149-476-341
; Sequence 341, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER APPLICATION NUMBER: 60/043, 666	EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043, 312	EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043, 313	EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043, 672	EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/043, 315	EARLIER FILING DATE: 1997-04-11	EARLIER APPLICATION NUMBER: 60/048, 974	EARLIER FILING DATE: 1997-06-06	EARLIER APPLICATION NUMBER: 60/056, 886	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 877	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 889	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 893	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 630	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 878	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 882	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 888	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 894	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 911	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 636	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 864	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 892	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 631	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/056, 910	EARLIER FILING DATE: 1997-08-22	EARLIER APPLICATION NUMBER: 60/047, 595	EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 599	EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 586	EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 590	EARLIER FILING DATE: 1997-05-23	EARLIER APPLICATION NUMBER: 60/047, 594	EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 3.1%; Score 7; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 APSLLLL 181
Db 2 APSLLLL 8

RESULT 11
US-09-461-325-484
; Sequence 484, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16

; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 484
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-484

Query Match 3.1%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 24 SLLLLLP 30

RESULT 12
US-10-012-542-484
; Sequence 484, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 484
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-012-542-484

Query Match 3.1%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 24 SLLLLLP 30

RESULT 13

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US-10-115-123-484
; Sequence 484, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G3OAP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 484
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-123-484

Query Match          3.1%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 SLLLLLP 183
DB 24 SLLLLLP 30
|||||

RESULT 14
US-09-248-796A-26807
; Sequence 26807, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26807
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26807

Query Match          3.1%; Score 7; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 ALLHRL 191
DB 75 ALLHRL 81
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US-09-621-976-3926
; Sequence 3926, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3926
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -22..-1
US-09-621-976-3926

Query Match          3.1%; Score 7; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 SLLLLLP 183
DB 7 SLLLLLP 13
|||||

Search completed: September 22, 2006, 19:01:54
Job time : 51 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:12:14 ; Search time 169 Seconds
(without alignments)
611.224 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTRWHVRLFTVSLAQII.....PSVLQRRRRCGRPLGRL 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 17010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA Main.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.psp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.psp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.psp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.psp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.psp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	223	100.0	223	4	US-10-665-602-2
2	223	100.0	229	3	US-09-764-893-98
3	223	100.0	229	3	US-09-764-881-101
4	223	100.0	229	3	US-09-764-853-608
5	223	100.0	229	3	US-09-764-898-269
6	223	100.0	229	3	US-09-764-881-101
7	223	100.0	229	4	US-10-073-865-98
8	223	100.0	229	4	US-10-242-747-101
9	187	83.9	223	4	US-10-295-027-422
10	187	83.9	223	4	US-10-295-027-1293
11	187	83.9	223	4	US-10-264-237-2712
12	187	83.9	223	5	US-10-940-431-4
13	187	83.9	231	3	US-09-764-898-198
14	145	65.0	223	4	US-10-257-113-2
15	15	6.7	202	5	US-10-940-431-3
16	9	4.0	157	4	US-10-425-115-351909
17	8	3.6	51	4	US-10-424-599-252112
18	8	3.6	51	4	US-10-437-963-124573
19	8	3.6	55	4	US-10-437-963-141814
20	8	3.6	55	4	US-10-425-115-249327
21	8	3.6	85	4	US-10-425-115-267412
22	8	3.6	105	4	US-10-437-963-180148
23	8	3.6	123	4	US-10-437-963-138083
24	8	3.6	149	6	US-11-096-568A-2904
25	8	3.6	158	6	US-11-097-143-32931
26	8	3.6	170	4	US-10-767-701-58031
27	8	3.6	180	3	US-09-860-670-131

28	8	3.6	180	4	US-10-227-646-131	Sequence 131, Appl
29	8	3.6	180	4	US-10-242-355-500	Sequence 500, Appl
30	8	3.6	209	6	US-11-096-568A-2903	Sequence 2903, Ap
31	8	3.6	209	6	US-11-096-568A-2905	Sequence 2905, Ap
32	8	3.6	349	4	US-10-437-963-114262	Sequence 114262, A
33	8	3.6	575	4	US-10-425-114-64569	Sequence 64569, A
34	8	3.6	575	4	US-10-425-114-68806	Sequence 68806, A
35	8	3.6	619	6	US-11-096-568A-19804	Sequence 19804, A
36	8	3.6	668	6	US-11-096-568A-19803	Sequence 19803, A
37	8	3.6	720	4	US-10-425-115-335408	Sequence 335408, A
38	8	3.6	720	6	US-11-096-568A-19802	Sequence 19802, A
39	8	3.6	721	4	US-10-437-963-202387	Sequence 202387, A
40	8	3.6	737	4	US-10-425-114-63855	Sequence 63855, A
41	8	3.6	1230	5	US-10-416-456A-1	Sequence 1, Appli
42	8	3.6	1253	5	US-10-450-763-54210	Sequence 54210, A
43	8	3.6	1718	4	US-10-415-188-6	Sequence 6, Appli
44	8	3.6	2524	4	US-10-190-115-25	Sequence 25, Appl
45	8	3.6	2524	4	US-10-369-072-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-10-665-602-2
; Sequence 2, Application US/10665602
; Publication No. US20040086967A1
; GENERAL INFORMATION:
; APPLICANT: Meissner, Paul S.
; Coleman, Timothy A.
; TITLE OF INVENTION: Human Cryptin Growth Factor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,602
; FILING DATE: 22-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,023A
; FILING DATE: 09-SEP-1999
; APPLICATION NUMBER: US 08/471,371
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marks, Michelle S.
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PF200D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-665-602-2

Query Match 100.0%; Score 223; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.4e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTWRHHVRLLLFTVSLALQIINLGSYQREKINGRGGEVTKVATQKHQSPLNWTS	SHFGE	60
Db	1	MTWRHHVRLLLFTVSLALQIINLGSYQREKINGRGGEVTKVATQKHQSPLNWTS	SHFGE	60
Qy	61	VTSGAEGWGPEPLPYSGRAFEGEGASAPRCRCNNGGTCVLGSCFCVCPAHFTGR	YCEHDQRR	120
Db	61	VTSGAEGWGPEPLPYSGRAFEGEGASAPRCRCNNGGTCVLGSCFCVCPAHFTGR	YCEHDQRR	120
Qy	121	SECGALEHGAWTLRACHLCRCIFGALHCLPIQTDPDRCDPKDFLASHAHGPSAG	CAAPSLLL	180
Db	121	SECGALEHGAWTLRACHLCRCIFGALHCLPIQTDPDRCDPKDFLASHAHGPSAG	CAAPSLLL	180
Qy	181	LIPCALLHRLRLPDPAPAHPRSLVPSVLQRRRRCGRFGLGHRL		223
Db	181	LIPCALLHRLRLPDPAPAHPRSLVPSVLQRRRRCGRFGLGHRL		223

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RESULT 2
US-09-764-893-98
; Sequence 98, Application US/09764893
; Publication No. US20020086330A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJO9
; CURRENT APPLICATION NUMBER: US/09/764,893
; CURRENT FILING DATE: 2001-01-19
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-893-98

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	Query Match	100.0%;	Score 223;	DB 3;	Length 229;
	Best Local Similarity	100.0%;	Prod. No. 1.5e-196;		
	Matches 223;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MTWRHHVRLFTVSLALQIINLNSGYQREKHNGRGVEVTKVATQKHRSPLNWTSSHFE	60		
Db	7	MTWRHHVRLFTVSLALQIINLNSGYQREKHNGRGVEVTKVATQKHRSPLNWTSSHFE	66		
Qy	61	VTSAEGWGPEEPLPYGRAFGEGASAPRCRNGGTCVLGSCFCVCPAHFTGRYCEHQRR	120		
Db	67	VTSAEGWGPEEPLPYGRAFGEGASAPRCRNGGTCVLGSCFCVCPAHFTGRYCEHQRR	126		
Qy	121	SEGCALPHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPDKDFLASHAHGSPGAGPSLLL	180		
Db	127	SEGCALPHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPDKDFLASHAHGSPGAGPSLLL	186		
Qy	181	LLPCALHRLRLRPDAPAPRSLVPSVLQRRRPPCGRFLGHRL	223		
Db	187	LLPCALHRLRLRPDAPAPRSLVPSVLQRRRPPCGRFLGHRL	229		

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RESULT 3
US-09-764-881-101
; Sequence 101, Application US/09764881
; Publication No. US20020086821A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ07
; CURRENT APPLICATION NUMBER: US/09/764.881

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; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-101

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Query Match	100.0%	Score 223;	DB 3;	Length 229;
Best Local Similarity	100.0%	Pred. No. 1.5e-196;		
Matches 223;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	MTWRHHVRLLF	TVSLAQII	NLGSYQREKHNGRGEVTKVATQKHRSPLNWTSSHFGE 60
Db	7	MTWRHHVRLLF	TVSLAQII	NLGSYQREKHNGRGEVTKVATQKHRSPLNWTSSHFGE 66
Qy	61	VTGSAEGWGPEE	PLPYSRAF	GEGASAPRCRNRGGTCVLGSCFCVCPAHFTGRYCEHDORR 120
Db	67	VTGSAEGWGPEE	PLPYSRAF	GEGASAPRCRNRGGTCVLGSCFCVCPAHFTGRYCEHDORR 126
Qy	121	SECGALEHGAWT	LRACHLRC	ICFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 180
Db	127	SECGALEHGAWT	LRACHLRC	ICFGALHCLPLQTPDRCDPKDFLASHAHGPSAGGAPSLLL 186
Qy	181	LLPCALLHRLR	LLRDPAPAH	PSRLVPSVLQRRRPPCGRFLGHRL 223
Db	187	LLPCALLHRLR	LLRDPAPAH	PSRLVPSVLQRRRPPCGRFLGHRL 229

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RESULT 4
US-09-764-853-608
; Sequence 608, Application US/09764853
; Patent No. US2002090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P3206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 608
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-608

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	Query Match	100.0%	Score 223	DB 3	Length 229
	Best Local Similarity	100.0%	Pred. No. 1.5e-196		
	Matches 223	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MTRRHVRLLFTVSLALQI	INLGNSYQREKNGRGGEVTKVATQKHROSPLNWTSSHGE	60	
Db	7	MTRRHVRLLFTVSLALQI	INLGNSYQREKNGRGGEVTKVATQKHROSPLNWTSSHGE	56	
Qy	61	VTSAEGWGPEEPYPYRAFGEGASAPRCCRNGGTCVLGSEFCVCPAHFTGRYCEHDQRR	120		


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Db 67 VTGAEGWGPEPLPYSAFEGEGASARPRCCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
Qy 121 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180
Db 127 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 186
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPLGHLRL 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPLGHLRL 229

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RESULT 5
 US-09-764-898-269
 ; Sequence 269, Application US/09764898
 ; Patent No. US20020090673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P201
 ; CURRENT APPLICATION NUMBER: US/09/764,898
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 311
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 269
 ; LENGTH: 229
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (2)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (3)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-764-898-269

Query Match 100.0%; Score 223; DB 3; Length 229;
 Best Local Similarity 100.0%; Pred. No. 1.5e-196;
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHQSPPLNWTSSHFGE 60
 Db 7 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHQSPPLNWTSSHFGE 66
 Qy 61 VTGAEGWGPEPLPYSAFEGEGASARPRCCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
 Db 67 VTGAEGWGPEPLPYSAFEGEGASARPRCCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
 Qy 121 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180
 Db 127 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 186
 Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPLGHLRL 223
 Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPLGHLRL 229

RESULT 6
 US-09-764-881-101
 ; Sequence 101, Application US/09764881
 ; Publication No. US20030125246A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P207
 ; CURRENT APPLICATION NUMBER: US/09/764,881
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 192
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 101

LENGTH: 229
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (2)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (3)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-764-881-101

Query Match 100.0%; Score 223; DB 3; Length 229;
 Best Local Similarity 100.0%; Pred. No. 1.5e-196;
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHQSPPLNWTSSHFGE 60
 Db 7 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHQSPPLNWTSSHFGE 66
 Qy 61 VTGAEGWGPEPLPYSAFEGEGASARPRCCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
 Db 67 VTGAEGWGPEPLPYSAFEGEGASARPRCCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
 Qy 121 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180
 Db 127 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 186
 Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPLGHLRL 223
 Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPLGHLRL 229

RESULT 7
 US-10-073-865-98
 ; Sequence 98, Application US/10073865
 ; Publication No. US20030044904A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P209C1
 ; CURRENT APPLICATION NUMBER: US/10/073,865
 ; CURRENT FILING DATE: 2002-02-14
 ; Prior Application removed - See file Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 154
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 98
 ; LENGTH: 229
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (2)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: misc_feature
 ; LOCATION: (3)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-10-073-865-98

Query Match 100.0%; Score 223; DB 4; Length 229;
 Best Local Similarity 100.0%; Pred. No. 1.5e-196;
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHQSPPLNWTSSHFGE 60
 Db 7 MTRHHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHQSPPLNWTSSHFGE 66
 Qy 61 VTGAEGWGPEPLPYSAFEGEGASARPRCCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
 Db 67 VTGAEGWGPEPLPYSAFEGEGASARPRCCNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
 Qy 121 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180

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Db      127  SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 186

Qy      181  LLPCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGRPGGLGHL 223
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Db      187  LLPCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGRPGGLGHL 229
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RESULT 8
US-10-242-747-101
; Sequence 101, Application US/10242747
; Publication No. US20040005577A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ07C1
; CURRENT APPLICATION NUMBER: US/10/242,747
; CURRENT FILING DATE: 2002-09-13
; PRIOR FILING DATE: 09/764,881
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2000-01-31
; PRIOR FILING DATE: 2000-01-31
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-06-28
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; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-07-26
; PRIOR FILING DATE: 2000-07-26
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-747-101

Query Match      100.0%; Score 223; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGVTKVATQKHQSPLNWTSSHFGE 60
        |||||
Db      7  MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGVTKVATQKHQSPLNWTSSHFGE 66
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Qy      61  VTGSAEGWGPEELPYSRATFEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
        |||||
Db      67  VTGSAEGWGPEELPYSRATFEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
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Qy      121  SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 180
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Db      127  SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGGAPSLLL 186
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Qy      181  LLPCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGRPGGLGHL 223
        |||||
Db      187  LLPCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGRPGGLGHL 229
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RESULT 9
US-10-295-027-422
; Sequence 422, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nacasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 2001-11-29
; PRIOR FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2002-01-08
; PRIOR FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 422
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-422

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Query Match      83.9%; Score 187; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.8e-163;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      37  EYTKVATQKHQSPLNWTSSHFGEVTSAGWGPEELPYSRATFEGASAPRCRNGGT 96
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Qy      97  CVLGSCFVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
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Qy      157  CDPKDFLASHAGPSAGGAPSLLLLPCCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGR 216
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Qy      217  PGLGHL 223
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Db      217  PGLGHL 223
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RESULT 10

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Db 97 CVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Qy 157 CDPKDFLASHAHGSPAGGAPSLLLLLPCALLHRLLRDPADPAHPRSLVPSVLQRRPCGR 216
Db 157 CDPKDFLASHAHGSPAGGAPSLLLLLPCALLHRLLRDPADPAHPRSLVPSVLQRRPCGR 216
Qy 217 PGLGHRL 223
Db 217 PGLGHRL 223

RESULT 13

US-09-764-898-198
; Sequence 198, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 198
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (44)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-198

Query Match 83.9%; Score 187; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.9e-163; Indels 0; Gaps 0;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 37 EVTKVATQKIQRSPLNWTSSHFGEVTSAGWGPEEPLPYSRAFEGEGASARPCCRNGGT 96
Db 45 EVTKVATQKIQRSPLNWTSSHFGEVTSAGWGPEEPLPYSRAFEGEGASARPCCRNGGT 104
Qy 97 CVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Db 105 CVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 164
Qy 157 CDPKDFLASHAHGSPAGGAPSLLLLLPCALLHRLLRDPADPAHPRSLVPSVLQRRPCGR 216
Db 165 CDPKDFLASHAHGSPAGGAPSLLLLLPCALLHRLLRDPADPAHPRSLVPSVLQRRPCGR 224
Qy 217 PGLGHRL 223
Db 225 PGLGHRL 231

RESULT 14

US-10-257-113-2
; Sequence 2, Application US/10257113
; Publication No. US20030207293A1
; GENERAL INFORMATION:
; APPLICANT: DUCKER, KLAUS
; TITLE OF INVENTION: CRYPTIC-LIKE SECRETED PROTEIN
; FILE REFERENCE: MERCK-2519
; CURRENT APPLICATION NUMBER: US/10/257,113
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: EP 00107142.2
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 223
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-257-113-2

Query Match 65.0%; Score 145; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-125;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 AFEGEGASARPCCRNGGTCVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHL 138
Db 79 AFEGEGASARPCCRNGGTCVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHL 138
Qy 139 CRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGGAPSLLLLLPCALLHRLLRDPADPAH 198
Db 139 CRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGGAPSLLLLLPCALLHRLLRDPADPAH 198
Qy 199 PRSLVPSVLQRRPCGRPGLGHRL 223
Db 199 PRSLVPSVLQRRPCGRPGLGHRL 223

RESULT 15

US-10-940-431-3
; Sequence 3, Application US/10940431
; Publication No. US20050208045A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie
; APPLICANT: Harrison, Craig A.
; APPLICANT: Gray, Peter C.
; TITLE OF INVENTION: CRYPTO Antagonism of Activin and TGF-
; TITLE OF INVENTION: Signaling
; FILE REFERENCE: D6525
; CURRENT APPLICATION NUMBER: US/10/940,431
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: 60/503,046
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Macintosh OS 10
; SEQ ID NO 3
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence of mouse Criptic protein
US-10-940-431-3

Query Match 6.7%; Score 15; DB 5; Length 202;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 NGGTCVLGSCVCPA 107
Db 101 NGGTCVLGSCVCPA 115

Search completed: September 22, 2006, 19:15:43
Job time : 171 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:13:04 ; Search time 34 seconds
(without alignment)
466.741 Million cell updates/sec

Title: US-10-665-602-2
Perfect score: 223
Sequence: 1 MTRWHRVLLFTVSLALQII.....PSVLQRRRRCGRGLGHL 223

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Gapop 60.0 , Gapext 60.0

Searched: 260401 seqs, 71162236 residues

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Total number of hits satisfying chosen parameters: 1506

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.6	105	6	US-10-449-902-29843
2	8	3.6	105	6	US-10-449-902-31212
3	8	3.6	105	6	US-10-449-902-32435
4	8	3.6	112	6	US-10-449-902-49548
5	8	3.6	149	6	US-10-953-349-18763
6	8	3.6	186	6	US-10-449-902-41657
7	8	3.6	209	6	US-10-953-349-18762
8	8	3.6	349	6	US-10-449-902-49942
9	8	3.6	349	6	US-10-449-902-50970
10	8	3.6	721	6	US-10-449-902-45561
11	8	3.6	721	6	US-10-449-902-48415
12	8	3.6	788	6	US-10-530-187-275
13	8	3.6	880	6	US-10-449-902-41116
14	7	3.1	50	7	US-11-155-989-716
15	7	3.1	51	7	US-11-155-989-715
16	7	3.1	52	7	US-11-155-989-713
17	7	3.1	73	6	US-10-449-902-38162
18	7	3.1	73	6	US-10-449-902-12304
19	7	3.1	107	6	US-11-155-989-805
20	7	3.1	109	7	US-11-155-989-805
21	7	3.1	112	7	US-11-155-989-462
22	7	3.1	119	6	US-10-196-749-140
23	7	3.1	119	6	US-10-525-116-1106
24	7	3.1	119	7	US-11-101-316-26
25	7	3.1	119	7	US-11-376-673-26

ALIGNMENTS

RESULT 1

US-10-449-902-29843
; Sequence 29843, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29843
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29843

Query Match 3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLILLLP 183
Db 42 PSLILLLP 49

RESULT 2

US-10-449-902-31212
; Sequence 31212, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269

Sequence 2, Appli
Sequence 2346, Ap
Sequence 14739, A
Sequence 60155, A
Sequence 272, App
Sequence 5464, Ap
Sequence 154, App
Sequence 14738, A
Sequence 14738, A
Sequence 6154, A
Sequence 46395, A
Sequence 95514, A
Sequence 14550, A
Sequence 18828, A
Sequence 26719, A
Sequence 47068, A
Sequence 48050, A
Sequence 53119, A
Sequence 36004, A
Sequence 169, App

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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31212
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31212

Query Match          3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 PSLLLLLP 183
Db 73 PSLLLLLP 80

RESULT 3
US-10-449-902-32435
; Sequence 32435, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32435
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32435

Query Match          3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 PSLLLLLP 183
Db 73 PSLLLLLP 80

RESULT 4
US-10-449-902-49548
; Sequence 49548, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 49548
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49548

Query Match          3.6%; Score 8; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 APSLLLLL 182
Db 45 APSLLLLL 52

RESULT 5
US-10-953-349-18763
; Sequence 18763, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18763
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18763

Query Match          3.6%; Score 8; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LFTVSLAL 17
Db 103 LFTVSLAL 110

RESULT 6
US-10-449-902-41657
; Sequence 41657, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41657
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41657

Query Match          3.6%; Score 8; DB 6; Length 186;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 ALLHRLLR 192
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Db      146 ALLHRLLR 153
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RESULT 7
US-10-953-349-18762
; Sequence 18762, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18762
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18762

Query Match      3.6%; Score 8; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LFTVSLAL 17
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Db      163 LFTVSLAL 170

RESULT 8
US-10-449-902-49942
; Sequence 49942, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49942
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49942

Query Match      3.6%; Score 8; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      176 PSLLLLLP 183
|||||
Db      4 PSLLLLLP 11

RESULT 9
US-10-449-902-50970
; Sequence 50970, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
```

```
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50970
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50970

Query Match      3.6%; Score 8; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      176 PSLLLLLP 183
|||||
Db      4 PSLLLLLP 11

RESULT 10
US-10-449-902-45561
; Sequence 45561, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45561
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45561

Query Match      3.6%; Score 8; DB 6; Length 721;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      185 ALLHRLLR 192
|||||
Db      107 ALLHRLLR 114

RESULT 11
US-10-449-902-48415
; Sequence 48415, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
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; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48415
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48415

Query Match          3.6%; Score 8; DB 6; Length 721;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 ALLHRLLR 192
DB 107 ALLHRLLR 114

RESULT 12
US-10-530-187-275
; Sequence 275, Application US/10530187
; Publication No. US20060183120A1
; GENERAL INFORMATION:
; APPLICANT: THE, Bin Tean
; APPLICANT: TAKAHASHI, Masayuki
; TITLE OF INVENTION: Molecular Subclassification of Kidney Tumors and the Discovery of
; TITLE OF INVENTION: New Diagnostic Markers
; FILE REFERENCE: 28927-0014
; CURRENT APPLICATION NUMBER: US/10/530,187
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031476
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US 60/415,775
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275
; LENGTH: 788
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-530-187-275

Query Match          3.6%; Score 8; DB 6; Length 788;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 APSLLLLL 182
DB 12 APSLLLLL 19

RESULT 13
US-10-449-902-41116
; Sequence 41116, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791

; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41116
; LENGTH: 880
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41116

Query Match          3.1%; Score 7; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 CGRPGLG 220
DB 38 CGRPGLG 44

RESULT 15
US-11-155-989-715
; Sequence 715, Application US/11155989
; Publication No. US20060177831A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Alba, Benjamin M.
; APPLICANT: Bakker, Alice
; APPLICANT: Duguay, Amy N.
; APPLICANT: Liu, Qiang
; APPLICANT: Silverman, Joshua
; APPLICANT: Smith, Richard
; APPLICANT: Avidia Research Institute
```



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; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001410US
; CURRENT APPLICATION NUMBER: US/11/155,989
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 10/957,351
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 925
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 715
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: c-Met-binding family 9 (Fam9)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (17)...(17)
; OTHER INFORMATION: Xaa = any amino acid
US-11-155-989-715

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Query Match      3.1%; Score 7; DB 7; Length 51;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      214 CGRPGLG 220
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Db       38 CGRPGLG 44

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Job time : 36 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 18:55:33 ; Search time 38 Seconds
(without alignments)
564.640 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTRWHVRLFTVSLALQII.....PSVLQRERRPCGRPLGRL 223

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Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_80:*
1: Pirl1.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.6	162	2 A72770	hypothetical prote
2	8	3.6	859	2 S61246	origin-binding pro
3	8	3.6	2524	2 A35844	Xotch protein - Af
4	7	3.1	22	2 PH1333	Ig heavy chain DJ
5	7	3.1	52	2 AF0293	hypothetical prote
6	7	3.1	76	2 AF1928	hypothetical prote
7	7	3.1	104	2 A10775	conserved hypothet
8	7	3.1	109	2 B70037	hypothetical prote
9	7	3.1	195	2 B83506	hypothetical prote
10	7	3.1	198	2 T26708	hypothetical prote
11	7	3.1	249	2 F87313	hydroxyacylglutath
12	7	3.1	264	2 F64896	probable membrane
13	7	3.1	264	2 H85733	probable transport
14	7	3.1	264	2 G90884	probable transport
15	7	3.1	269	2 E95999	probable methyl-tr
16	7	3.1	291	2 I39737	hypothetical prote
17	7	3.1	291	2 T23595	hypothetical prote
18	7	3.1	293	2 B64880	probable multiple
19	7	3.1	293	2 B90865	hypothetical prote
20	7	3.1	293	2 G85753	hypothetical prote
21	7	3.1	294	2 B71256	conserved hypothet
22	7	3.1	296	2 T04703	hypothetical prote
23	7	3.1	304	2 A33274	insulin-like growt
24	7	3.1	305	2 JN0508	insulin-like growt
25	7	3.1	305	2 I48601	insulin-like growt
26	7	3.1	312	2 I78664	hypothetical prote
27	7	3.1	312	2 H91237	hypothetical prote
28	7	3.1	312	2 D86085	hypothetical prote
29	7	3.1	322	2 H87111	probable transcrip

30	7	3.1	333	1 HLHUCB	T-cell surface gly
31	7	3.1	352	2 T06935	photosystem II pro
32	7	3.1	366	1 A40056	inhibin alpha chai
33	7	3.1	374	2 B96737	hypothetical prote
34	7	3.1	380	2 J25579	manganese peroxida
35	7	3.1	385	2 T24324	hypothetical prote
36	7	3.1	390	2 F86461	F14M2.7 protein -
37	7	3.1	411	2 A75479	citrate synthase -
38	7	3.1	421	2 T35205	citrate synthase-1
39	7	3.1	434	2 S25958	gene coxI intron 4
40	7	3.1	446	2 T10103	cytochrome-c oxida
41	7	3.1	471	2 T43803	cytochrome-c oxida
42	7	3.1	508	2 S74200	cytochrome-c oxida
43	7	3.1	510	2 H87320	conserved hypothet
44	7	3.1	513	1 ODHU1	cytochrome-c oxida
45	7	3.1	514	2 S29810	monoamine transpor

ALIGNMENTS

RESULT 1

A72770

hypothetical protein APE0148 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Sep-2000

C;Accession: A72770

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: A72770

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-162 <KAW>

A;Cross-references: UNIPARC:UPI000005DA13; DDBJ:AP0000058; NID:G5103388; PIDN:BAA79059.1;

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE0148

C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0024

Query Match	3.6%	Score 8;	DB 2;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 3.8;		
Matches	8;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
				0;

Qy 14 SLALQIIN 21

Db 4 SLALQIIN 11

RESULT 2

S61246

origin-binding protein - bovine herpesvirus 1

C;Species: bovine herpesvirus 1

C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004

C;Accession: S61246

R;Vicek, C.; Benes, V.; Lu, Z.; Kutish, G.F.; Paces, V.; Rock, D.; Letchworth, G.J.; Sch

submitted to the EMBL Data Library, January 1995

A;Description: Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus

A;Reference number: S61233

A;Accession: S61246

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-859 <VLC>

A;Cross-references: UNIPROT:P52377; UNIPARC:UPI0000130B97; EMBL:Z48053; NID:g971311; PID:

C;Superfamily: varicella-zoster virus gene 51 protein

Query Match 3.6%; Score 8; DB 2; Length 859;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 ALLHRLLR 192

```

Db      198 ALLHRLLR 205
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RESULT 3
A35844
Xotch protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 05-Oct-2004
C;Accession: A35844
R;Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID:90385285; PMID:2402639
A;Accession: A35844
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-2524 <COF>
A;Cross-references: UNIPARC:UPI000004F253
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: transmembrane protein
F;146-177/Domain: EGF homology <EGX1>
F;184-215/Domain: EGF homology <EGF1>
F;222-254/Domain: EGF homology <EGF>
F;456-487/Domain: EGF homology <EGX2>
F;757-788/Domain: EGF homology <EGF3>
F;1025-1056/Domain: EGF homology <EGX3>
F;1924-1956/Domain: ankyrin repeat homology <AN1>
F;1957-1989/Domain: ankyrin repeat homology <AN2>
F;1991-2023/Domain: ankyrin repeat homology <AN3>
F;2024-2056/Domain: ankyrin repeat homology <AN4>
F;2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match      3.6%; Score 8; DB 2; Length 2524;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      91 CRNGGTCV 98
|||||
Db      266 CRNGGTCV 273

RESULT 4
PH1333
Ig heavy chain DJ region (clone C238-133) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1333
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1333
A;Molecule type: DNA
A;Residues: 1-22 <WAS>
A;Cross-references: UNIPARC:UPI000017C236
C;Keywords: heterotetramer; immunoglobulin

Query Match      3.1%; Score 7; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      177 SLLLLLP 183
|||||
Db      8 SLLLLLP 14

RESULT 5
AF0293
hypothetical protein YP02405 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0293

```

```

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ii, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0293
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52 <KUR>
A;Cross-references: UNIPROT:Q8ZDY9; UNIPARC:UPI00000CD90A; GB:AL590842; PIDN:CAC91210.1;
C;Genetics:
A;Gene: YP02405

Query Match      3.1%; Score 7; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      177 SLLLLLP 183
|||||
Db      36 SLLLLLP 42

RESULT 6
AF1928
hypothetical protein asl0977 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF1928
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF1928
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-76 <KUR>
A;Cross-references: UNIPROT:Q8YV74; UNIPARC:UPI00000CDF33; GB:BA000019; PIDN:BAB72934.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asl0977

Query Match      3.1%; Score 7; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      178 LLLLLLP 184
|||||
Db      8 LLLLLLP 14

RESULT 7
AI0775
conserved hypothetical protein yohN [imported] - Salmonella enterica subsp. enterica sero
C;Species: Salmonella enterica subsp. enterica serovar typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0775
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, F.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0775
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104 <PAR>
A;Cross-references: UNIPARC:UPI0000059BFD; GB:AL513382; PIDN:CAD02527.1; PID:gl6503388; C
C;Genetics:

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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

Search completed: September 22, 2006, 19:01:00
Job time : 41 secs